



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/684,383

DATE: 06/06/2002  
TIME: 16:17:16

Input Set : N:\Crf3\RULE60\09684383.raw  
Output Set: N:\CRF3\06062002\I684383.raw

# SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: H TTEN, Gertrud  
6 NEIDHARDT, Helge  
7 BECHTOLD, Rolf  
8 POHL, Jens  
9 PAULISTA, Michael

11 (ii) TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE  
12 TGF- FAMILY

14 (iii) NUMBER OF SEQUENCES: 49

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP  
18 (B) STREET: 655 Fifteenth Street, N. W., G Street Lobby,  
19 Suite 330

20 (C) CITY: Washington

21 (D) STATE: DC

22 (E) COUNTRY: USA

23 (F) ZIP: 20005

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/684,383

C--> 33 (B) FILING DATE: 10-Oct-2000

43 (C) CLASSIFICATION:

65 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/09/218,176

38 (B) FILING DATE:

41 (A) APPLICATION NUMBER: 08/679,048

42 (B) FILING DATE: 12-JUL-1996

46 (A) APPLICATION NUMBER: PCT/EP96/03065

47 (B) FILING DATE: 12-JUL-1996

50 (A) APPLICATION NUMBER: PCT/EP93/00350

51 (B) FILING DATE: 2-FEB-1993

54 (A) APPLICATION NUMBER: US 08/482,577

55 (B) FILING DATE: 7-JUN-1995

58 (A) APPLICATION NUMBER: EP 92 102 324.8

59 (B) FILING DATE: 12-FEB-1992

62 (A) APPLICATION NUMBER: DE P 44 23 190.3

63 (B) FILING DATE: 01-JUL-1994

66 (A) APPLICATION NUMBER: DE 195 11 243.1

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67      (B) FILING DATE: 27-MAR-1995
70      (viii) ATTORNEY/AGENT INFORMATION:
71          (A) NAME: KITTS, Monica Chin
72          (B) REGISTRATION NUMBER: 36,105
73          (C) REFERENCE/DOCKET NUMBER: P564-6010
75      (ix) TELECOMMUNICATION INFORMATION:
76          (A) TELEPHONE: 202/638-5000
77          (B) TELEFAX: 202/638-4810
79      (2) INFORMATION FOR SEQ ID NO: 1:
80          (i) SEQUENCE CHARACTERISTICS:
81              (A) LENGTH: 2272 base pairs
82              (B) TYPE: nucleic acid
83              (C) STRANDEDNESS: single
84              (D) TOPOLOGY: linear
W--> 86          (ii) MOLECULE TYPE: DNA
87          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
88      CAAGGAGCCA TGCCAGCTGG ACACACACTT CTTCCAGGGC CTCTGGCAGC CAGGACAGAG      60
89      TTGAGACCAC AGCTGTTGAG ACCCTGAGCC CTGAGTCTGT ATTGCTCAAG AAGGGCCTTC      120
90      CCCAGCAATG ACCTCCTCAT TGCTTCTGGC CTTTCTCCTC CTGGCTCCAA CCACAGTGGC      180
91      CACTCCCAGA GCTGGCGGTC AGTGTCAGC ATGTGGGGGG CCCACCTTGG AACTGGAGAG      240
92      CCAGCGGGAG CTGCTTCTTG ATCTGGCCAA GAGAAGCATC TTGGACAAGC TGCACCTCAC      300
93      CCAGCGCCCA AACTGAACC GCCCTGTGTC CAGAGCTGCT TTGAGGACTG CACTGCAGCA      360
94      CCTCCACGGG GTCCACAGG GGGCACTTCT AGAGGACAAC AGGGAACAGG AATGTGAAAT      420
95      CATCAGCTTT GCTGAGACAG GCCTCTCCAC CATCAACCAG ACTCGTCTTG ATTTTCACTT      480
96      CTCCTCTGAT AGAACTGCTG GTGACAGGGA GGTCCAGCAG GCCAGTCTCA TGTTCTTTGT      540
97      GCAGCTCCCT TCCAATACCA CTTGGACCTT GAAAGTGAGA GTCCTTGTGC TGGGTCCACA      600
98      TAATACCAAC CTCACCTTGG CTACTCAGTA CCTGCTGGAG GTGGATGCCA GTGGCTGGCA      660
99      TCAACTCCCC CTAGGGCCTG AAGCTCAAGC TGCCTGCAGC CAGGGGCACC TGACCCTGGA      720
100     GCTGGTACTT GAAGGCCAGG TAGCCCAGAG CTCAGTCATC CTGGGTGGAG CTGCCCATAG      780
101     GCCTTTTGTG GCAGCCCGGG TGAGAGTTGG GGGCAAACAC CAGATTCACC GACGAGGCAT      840
102     CGACTGCCAA GGAGGGTCCA GGATGTGCTG TCGACAAGAG TTTTGTGG ACTTCCGTGA      900
103     GATTGGCTGG CACGACTGGA TCATCCAGCC TGAGGGCTAC GCCATGAACT TCTGCATAGG      960
104     GCAGTGCCCA CTACACATAG CAGGCATGCC TGGTATTGCT GCCTCCTTTC AACTGCAGT      1020
105     GCTCAATCTT CTAAGGCCA ACACAGCTGC AGGCACCACT GGAGGGGGCT CATGCTGTGT      1080
106     ACCCACGGCC CGGCGCCCCC TGTCTCTGCT CTATTATGAC AGGGACAGCA ACATTGTCAA      1140
107     GACTGACATA CCTGACATGG TAGTAGAGGC CTGTGGGTGC AGTTAGTCTA TGTGTGGTAT      1200
108     GGGCAGCCCA AGGTTGCATG GGAAAACACG CCCCTACAGA AGTGCACTC CTGAGAGGA      1260
109     GGGAATGACC TCATTCTCTG TCCAGAATGT GGAATCCCTC TTCCTGAGCA TCTTATGGAA      1320
110     ATTACCCAC CTTTGACTTG AAGAAACCTT CATCTAAAGC AAGTCACTGT GCCATCTTCC      1380
111     TGACCACTAC CCTCTTTCCT AGGGCATAGT CCATCCCGCT AGTCCATCCC GCTAGCCCCA      1440
112     CTCCAGGGAC TCAGACCCAT CTCCAACCAT GAGCAATGCC ATCTGGTTCC CAGGCAAAGA      1500
113     CACCCTTAGC TCACCTTTAA TAGACCCCAT AACCCTACTAT GCCTTCCTGT CCTTCTACT      1560
114     CAATGGTCCC CACTCCAAGA TGAGTTGACA CAACCCCTTC CCCCAATTTT TGTGGATCTC      1620
115     CAGAGAGGCC CTTCTTTTGA TTCACCAAAG TTTAGATCAC TGCTGCCAA AATAGAGGCT      1680
116     TACCTACCCC CCTCTTTGTT GTGAGCCCTT GTCCTTCTTA GTTGTCAGG TGAATACTA      1740
117     AAGCTCTCTT TGCATACCTT CATCCATTTT TTGTCCTTCT CTGCCTTCT CTATGCCCTT      1800
118     AAGGGGTGAC TTGCCTGAGC TCTATCACCT GAGCTCCCTT GCCCTCTGGC TTCCTGCTGA      1860
119     GGTCAGGGCA TTTCTTATCC CTGTTCCTC TCTGTCTAGG TGTCATGGTT CTGTGTAAGT      1920
120     GTGGCTATTC TGTGTCCCTA CACTACCTGG CTACCCCTT CCATGGCCCC AGCTCTGCCT      1980

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158 ACATTCTGAT TTTTTTTTTT TTTTTTTTTT TGAAAAGTTA AAAATTCCTT AATTTTTTAT 2040
160 TCCTGGTACC ACTACCACAA TTTACAGGGC AATATACCTG ATGTAATGAA AAGAAAAAGA 2100
162 AAAAGACAAA GCTACAACAG ATAAAAGACC TCAGGAATGT ACATCTAATT GACACTACAT 2160
164 TGCATTAATC AATAGCTGCA CTTTTTGCAA ACTGTGGCTA TGACAGTCCT GAACAAGAAG 2220
166 GGTTTCCTGT TTAAGCTGCA GTAACTTTC TGACTATGGA TCATCGTTCC TT 2272

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168 (2) INFORMATION FOR SEQ ID NO: 2:

170 (i) SEQUENCE CHARACTERISTICS:

171 (A) LENGTH: 352 amino acids

172 (B) TYPE: amino acid

173 (C) STRANDEDNESS: single

174 (D) TOPOLOGY: linear

176 (ii) MOLECULE TYPE: peptide

179 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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181 Met Thr Ser Ser Leu Leu Leu Ala Phe Leu Leu Leu Ala Pro Thr Thr
182 1 5 10 15
184 Val Ala Thr Pro Arg Ala Gly Gly Gln Cys Pro Ala Cys Gly Gly Pro
185 20 25 30
187 Thr Leu Glu Leu Glu Ser Gln Arg Glu Leu Leu Leu Asp Leu Ala Lys
188 35 40 45
190 Arg Ser Ile Leu Asp Lys Leu His Leu Thr Gln Arg Pro Thr Leu Asn
191 50 55 60
193 Arg Pro Val Ser Arg Ala Ala Leu Arg Thr Ala Leu Gln His Leu His
194 65 70 75 80
196 Gly Val Pro Gln Gly Ala Leu Leu Glu Asp Asn Arg Glu Gln Glu Cys
197 85 90 95
199 Glu Ile Ile Ser Phe Ala Glu Thr Gly Leu Ser Thr Ile Asn Gln Thr
200 100 105 110
202 Arg Leu Asp Phe His Phe Ser Ser Asp Arg Thr Ala Gly Asp Arg Glu
203 115 120 125
205 Val Gln Gln Ala Ser Leu Met Phe Phe Val Gln Leu Pro Ser Asn Thr
206 130 135 140
208 Thr Trp Thr Leu Lys Val Arg Val Leu Val Leu Gly Pro His Asn Thr
209 145 150 155 160
211 Asn Leu Thr Leu Ala Thr Gln Tyr Leu Leu Glu Val Asp Ala Ser Gly
212 165 170 175
214 Trp His Gln Leu Pro Leu Gly Pro Glu Ala Gln Ala Ala Cys Ser Gln
215 180 185 190
217 Gly His Leu Thr Leu Glu Leu Val Leu Glu Gly Gln Val Ala Gln Ser
218 195 200 205
220 Ser Val Ile Leu Gly Gly Ala Ala His Arg Pro Phe Val Ala Ala Arg
221 210 215 220
223 Val Arg Val Gly Gly Lys His Gln Ile His Arg Arg Gly Ile Asp Cys
224 225 230 235 240
226 Gln Gly Gly Ser Arg Met Cys Cys Arg Gln Glu Phe Phe Val Asp Phe
227 245 250 255
229 Arg Glu Ile Gly Trp His Asp Trp Ile Ile Gln Pro Glu Gly Tyr Ala
230 260 265 270
232 Met Asn Phe Cys Ile Gly Gln Cys Pro Leu His Ile Ala Gly Met Pro
233 275 280 285

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235 Gly Ile Ala Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala  
 236 290 295 300  
 238 Asn Thr Ala Ala Gly Thr Thr Gly Gly Gly Ser Cys Cys Val Pro Thr  
 239 305 310 315 320  
 241 Ala Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile  
 242 325 330 335  
 244 Val Lys Thr Asp Ile Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser  
 245 340 345 350

248 (2) INFORMATION FOR SEQ ID NO: 3:

250 (i) SEQUENCE CHARACTERISTICS:

251 (A) LENGTH: 1558 base pairs

252 (B) TYPE: nucleic acid

253 (C) STRANDEDNESS: single

254 (D) TOPOLOGY: linear

W--&gt; 256 (ii) MOLECULE TYPE: DNA

259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

261 AAGGAGTCAT GCCAGTCGGA GGTCAGTCAC ATTCCTCCCA GGGTCCCTGG TGCCCAGGAC 60  
 262 AGAGTTGAAG CACTCCCGTT GAGACCCCTGA ATATAGGCTT TGGGTCCTTT AAGGAGGCTA 120  
 263 TCCTCCAGCA ATGGCCTCCT CCTTGCTCCT GGCTCTTCTG TTCCTGACTC CAACCACAGT 180  
 264 AGTGAACCCC AAAACTGAGG GTCCATGCCC AGCATGTTGG GGTGCCATCT TTGACCTGGA 240  
 265 GAGCCAGCGG GAGCTGCTTC TCGATTTGGC CAAGAAAAGT ATCCTGGACA AGCTGCACCT 300  
 266 CAGCCAGCGC CCCATACTCA GTCGGCCAGT GTCCAGAGGG GCTCTCAAGA CCGCGCTGCA 360  
 267 GCGCCTCCGC GGGCCTCGAC GGGAAACCCCT GTTGGAGCAT GACCAGAGAC AAGAAGAATA 420  
 268 TGAGATCATC AGCTTTGCTG ACACAGACCT CTCCAGCATC AACCAGACCC GGCTCGAGTT 480  
 269 CCACTTCTCT GGTAGAATGG CCAGTGGCAT GGAGGTCCGG CAGACCCGCT TCATGTTCTT 540  
 270 CGTGCACTTC CCCACAATG CCACCCAGAC CATGAATATA AGAGTTCTTG TGCTAAGACC 600  
 271 ATATGACACC AACCTCACCT TGACAAGTCA GTACGTGGTG CAGGTGAATG CCAGTGGCTG 660  
 272 GTACCAGCTT CTCCTGGGAC CTGAAGCTCA AGCTGCTTGC AGCCAGGGAC ACCTTACTCT 720  
 273 GGAGCTGGTA CCAGAAAGCC AGGTGGCCCA CAGTTCCTTG ATCCTGGGCT GGTTTTCCCA 780  
 274 CAGGCCTTTT GTGGCAGCCC AGGTAAGGGT TGAGGGCAAG CATCGGGTTC GCCGGCGAGG 840  
 275 TATCGATTGC CAGGGGGGGT CCAGGATGTG CTGTCGACAA GAGTTTTTTG TAGACTTCCG 900  
 276 TGAGATTGGC TGGAATGACT GGATCATCCA GCCTGAAGGC TATGCCATGA ACTTCTGCAC 960  
 277 TGGGCAGTGC CCACTACATG TGGCAGGCAT GCCTGGCATC TCTGCCTCCT TTCACACTGC 1020  
 278 AGTGCTGAAT CTGCTCAAAG CCAACGCAGC TGCTGGCACC ACTGGCAGGG GCTCGTGTG 1080  
 279 CGTGCCCTACA TCTCGGCGCC CTCTGTCTTT GCTCTACTAT GACAGGGACA GCAACATTGT 1140  
 280 CAAGACGGAT ATACCTGACA TGGTGGTCGA GGCCTGCGGG TGTAGTTAGC TTATGGGTGA 1200  
 281 TACAGGCTGC CTGAGGTAGA ATGGCCTTCC TCAGGAAGGG AAACCTCTGT CCCACTTCTG 1260  
 282 TCCAGAATGG AAACACCTTT CTAAGCATGC AGACATCCCT CTGTGGACTT CAGGGGATCC 1320  
 283 ACCTCTAAAG AGAGTCACTA GTGACCAACA GCCTTTCTCT CTCCTGGGAC ATGGTTGACC 1380  
 284 CAGTACACCC ATCCTCAGCC TTAAGTTAGA GGCTAATCGA CTCCTACATA TATATGTCAT 1440  
 285 TTTGTCTTAG CAAACACCCC TTAGCTCCCC TTAGTCAACT ATGTAATCTA CTCTGCCTCC 1500  
 286 CTGACCCCTGC CACCGGAAGG TTCCTATTCC ACGATGATAT GCCTTAGTGT CTCCCCTT 1558

288 (2) INFORMATION FOR SEQ ID NO: 4:

289 (i) SEQUENCE CHARACTERISTICS:

290 (A) LENGTH: 352 amino acids

291 (B) TYPE: amino acid

292 (C) STRANDEDNESS: single

293 (D) TOPOLOGY: linear

295 (ii) MOLECULE TYPE: peptide

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299      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
301 Met Ala Ser Ser Leu Leu Leu Ala Leu Leu Phe Leu Thr Pro Thr Thr
302 1          5          10          15
304 Val Val Asn Pro Lys Thr Glu Gly Pro Cys Pro Ala Cys Trp Gly Ala
305          20          25          30
307 Ile Phe Asp Leu Glu Ser Gln Arg Glu Leu Leu Leu Asp Leu Ala Lys
308          35          40          45
310 Lys Ser Ile Leu Asp Lys Leu His Leu Ser Gln Arg Pro Ile Leu Ser
311          50          55          60
313 Arg Pro Val Ser Arg Gly Ala Leu Lys Thr Ala Leu Gln Arg Leu Arg
314 65          70          75          80
316 Gly Pro Arg Arg Glu Thr Leu Leu Glu His Asp Gln Arg Gln Glu Glu
317          85          90          95
319 Tyr Glu Ile Ile Ser Phe Ala Asp Thr Asp Leu Ser Ser Ile Asn Gln
320          100          105          110
322 Thr Arg Leu Glu Phe His Phe Ser Gly Arg Met Ala Ser Gly Met Glu
323          115          120          125
325 Val Arg Gln Thr Arg Phe Met Phe Phe Val Gln Phe Pro His Asn Ala
326          130          135          140
328 Thr Gln Thr Met Asn Ile Arg Val Leu Val Leu Arg Pro Tyr Asp Thr
329 145          150          155          160
331 Asn Leu Thr Leu Thr Ser Gln Tyr Val Val Gln Val Asn Ala Ser Gly
332          165          170          175
334 Trp Tyr Gln Leu Leu Leu Gly Pro Glu Ala Gln Ala Ala Cys Ser Gln
335          180          185          190
337 Gly His Leu Thr Leu Glu Leu Val Pro Glu Ser Gln Val Ala His Ser
338          195          200          205
340 Ser Leu Ile Leu Gly Trp Phe Ser His Arg Pro Phe Val Ala Ala Gln
341          210          215          220
343 Val Arg Val Glu Gly Lys His Arg Val Arg Arg Arg Gly Ile Asp Cys
344 225          230          235          240
346 Gln Gly Gly Ser Arg Met Cys Cys Arg Gln Glu Phe Phe Val Asp Phe
347          245          250          255
349 Arg Glu Ile Gly Trp Asn Asp Trp Ile Ile Gln Pro Glu Gly Tyr Ala
350          260          265          270
352 Met Asn Phe Cys Thr Gly Gln Cys Pro Leu His Val Ala Gly Met Pro
353          275          280          285
355 Gly Ile Ser Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala
356          290          295          300
358 Asn Ala Ala Ala Gly Thr Thr Gly Arg Gly Ser Cys Cys Val Pro Thr
359 305          310          315          320
361 Ser Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile
362          325          330          335
364 Val Lys Thr Asp Ile Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser
365          340          345          350
368 (2) INFORMATION FOR SEQ ID NO: 5:
370      (i) SEQUENCE CHARACTERISTICS:
371          (A) LENGTH: 18 base pairs
372          (B) TYPE: nucleic acid

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/684,383

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Input Set : N:\Crf3\RULE60\09684383.raw

Output Set: N:\CRF3\06062002\I684383.raw

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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
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L:256 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3  
L:376 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5  
L:394 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
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L:1202 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=49